the core sequence of an alpha chain of the laminin family. This sequence is sufficient, for example, to recognize an integrin receptor which mediates, inter alia, the endocytosis of viral particles, for example of adenovirus. The P1 peptide binds irrespective of its conformation (linear or circular) to the integrin receptor. According to the present invention, the coding DNA sequence of the P1 peptide is inserted into the gene coding for an AAV

B1

Please replace the first full paragraph on page 11 with the following paragraph re-written in clean form:

In a further preferred embodiment, one or more insertions are present in the VP3 structural protein (Rutledge, E.A. et al. (1998) supra) before and/or after at least one amino acid in the sequence selected from, YKQIS SQSGA (SEQ ID NO: 2), YLTLN NGSQA (SEQ ID NO: 3), YYLSR TNTPS (SEQ ID NO: 4), EEKFF PQSGV (SEQ ID NO: 5), NPVAT EQYGS (SEQ ID NO: 6), LQRGN RQAAT (SEQ ID NO: 7), NVDFT VDTNG (SEQ ID NO: 8), because these sites are located on the exposed sites of a loop, in which case the risk of changing the VP3 structure is low.

B2

Please replace the first full paragraph on page 17 with the following paragraph re-written in clean form:

2. Mutations in VP3

a) ins447; YYLS**R** TNTPS (CPV: 300) (SEQ ID NO: 4)

B3

b) INS534; EEKFF PQSGV (CPV: 390) (SEQ ID NO: 5)

c) ins573; NPVAT EQYGS (CPV: 426) (SEQ ID NO: 6)

d) ins587; LQRGN RQAAT (CPV: 440) (SEQ ID NO: 7)

B3 e) ins713; NVDFT VDTNG (CPV: 565) (SEQ ID NO: 8)

CPV means here the location in the equivalent CPV capsid

(Named according to the number of amino acids (AAs) counted after the AA at the start of the N terminus in the VP-1 of AAV2, flanked by in each case 5 amino acids located N-terminally thereof and 5 amino acids located C-terminally thereof; the AA after which the insertion was introduced is shown bold).

Please replace the last paragraph on page 19 with the following paragraph re-written in clean form:

B4 The initial staring point was a plasmid pUC-AV2 which was prepared by subcoloning of the 4.8 kb BglII fragment of pAV2 (ATCC 37261, ref. 53) into the BamHI cleavage site of pUC19 (New England BioLabs Inc.). Mutations were carried out at defined sites in the plasmid by means of PCR-assisted mutagenesis known to the skilled person. This entailed a sequence coding for P1, a 14 AA peptide with the AA sequence, QAGTFALRGDNPQG (SEQ ID NO: 1), which contains the RGD binding motif of a laminin fragment (Aumailly et al. (1990) FEBS Lett. 262, 82-86), being inserted after nucleotides 3543, 3804, 3921, and 3963. This corresponds to an insertion after amino acids 447, 534, 573, and 587 of the AAV2 capsid protein (named according